



SEQUENCE LISTING

Lorz, et al

<120> NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT AND WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH

<130> AGR 1998/M 205/ FLH514413-3848

<140> 09/674,824

<141> 2000-11-06

<150> PCT/EP99/03156

<151> 1999-05-07

<150> DE 198 20607.0

<151> 1998-05-08

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 2771

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (280)..(2547)

<400> 1

cgccactcca ctgccttgc cccactccca ctcttctctc cccgcgcaca ccgagtcggc 60
accggctcat caccatcac ctgcggctcg gccaccggca aacccccga tccgcttttg 120
caggcagcgc actaaaaccc cggggagcgc gccccgcggc agcagcagca ccgcagtggg 180
agagagagggc ttcgccccgg cccgcaccga gcggggcgat ccaccgtccg tgcgtccgca 240
ctctctccgc ctctctccct gtcccgcgcg cccacaccc atg gcg gcg acg ggc 294
Met Ala Ala Thr Gly
1 5
gtc ggc gcc ggg tgc ctc gcc ccc agc gtc cgc ctg cgc gcc gat ccg 342
Val Gly Ala Gly Cys Leu Ala Pro Ser Val Arg Leu Arg Ala Asp Pro
10 15 20
gcg acg gcg gcc cgg gcg tcc gcc tgc gtc gtc cgc gcg cgg ctc cgg 390
Ala Thr Ala Ala Arg Ala Ser Ala Cys Val Val Arg Ala Arg Leu Arg
25 30 35
cgc ttg gcg cgg ggc cgc tac gtc gcc gag ctc agc agg gag ggc ccc 438
Arg Leu Ala Arg Gly Arg Tyr Val Ala Glu Leu Ser Arg Glu Gly Pro
40 45 50
gcg gcg cgc ccc gcg cag cag cag caa ctg gcc ccg ccg ctc gtg cca 486
Ala Ala Arg Pro Ala Gln Gln Gln Gln Leu Ala Pro Pro Leu Val Pro
55 60 65
ggc ttc ctc gcg ccg ccg ccg ccc gcg ccc gcc cag tcg ccg gcc ccg 534
Gly Phe Leu Ala Pro Pro Pro Pro Ala Gln Ser Pro Ala Pro
70 75 80 85

Sequence Listing

acg cag ccg ccc ctg ccg gac gcc ggc gtg ggg gaa ctc gcg ccc gac 582
 Thr Gln Pro Pro Leu Pro Asp Ala Gly Val Gly Glu Leu Ala Pro Asp
 90 95 100

ctc ctg ctc gaa ggg att gct gag gat tcc atc gac agc ata att gtg 630
 Leu Leu Leu Glu Gly Ile Ala Glu Asp Ser Ile Asp Ser Ile Ile Val
 105 110 115

gct gca agt gag cag gat tct gag atc atg gat gcg aat gag caa cct 678
 Ala Ala Ser Glu Gln Asp Ser Glu Ile Met Asp Ala Asn Glu Gln Pro
 120 125 130

caa gct aaa gtt aca cgt agc atc gtg ttt gtg act ggt gaa gct gct 726
 Gln Ala Lys Val Thr Arg Ser Ile Val Phe Val Thr Gly Glu Ala Ala
 135 140 145

cct tat gca aag tca ggg ggg ttg gga gat gtt tgt ggt tgc tta cca 774
 Pro Tyr Ala Lys Ser Gly Gly Leu Gly Asp Val Cys Gly Ser Leu Pro
 150 155 160 165

att gct ctt gct gct cgt ggt cac cga gtg atg gtt gta atg cca aga 822
 Ile Ala Leu Ala Ala Arg Gly His Arg Val Met Val Val Met Pro Arg
 170 175 180

tac tta aat ggg tcc tct gat aaa aac tat gca aag gca tta tac act 870
 Tyr Leu Asn Gly Ser Ser Asp Lys Asn Tyr Ala Lys Ala Leu Tyr Thr
 185 190 195

gcg aag cac att aag att cca tgc ttt ggg gga tca cat gaa gtg acc 918
 Ala Lys His Ile Lys Ile Pro Cys Phe Gly Gly Ser His Glu Val Thr
 200 205 210

ttt ttt cat gag tat aga gac aac gtc gat tgg gtg ttt gtc gat cat 966
 Phe Phe His Glu Tyr Arg Asp Asn Val Asp Trp Val Phe Val Asp His
 215 220 225

ccg tca tat cac aga cca gga agt tta tat gga gat aat ttt ggt gct 1014
 Pro Ser Tyr His Arg Pro Gly Ser Leu Tyr Gly Asp Asn Phe Gly Ala
 230 235 240 245

ttt ggt gat aat cag ttc aga tac aca ctc ctt tgc tat gct gca tgc 1062
 Phe Gly Asp Asn Gln Phe Arg Tyr Thr Leu Leu Cys Tyr Ala Ala Cys
 250 255 260

gag gcc cca cta atc ctt gaa ttg gga gga tat att tat gga cag aat 1110
 Glu Ala Pro Leu Ile Leu Glu Leu Gly Gly Tyr Ile Tyr Gly Gln Asn
 265 270 275

tgc atg ttt gtt gtg aac gat tgg cat gcc agc ctt gtg cca gtc ctt 1158
 Cys Met Phe Val Val Asn Asp Trp His Ala Ser Leu Val Pro Val Leu
 280 285 290

ctt gct gca aaa tat aga cca tac ggt gtt tac aga gat tcc cgc agc 1206
 Leu Ala Ala Lys Tyr Arg Pro Tyr Gly Val Tyr Arg Asp Ser Arg Ser
 295 300 305

acc ctt gtt ata cat aat tta gca cat cag ggt gtg gag cct gca agt 1254
 Thr Leu Val Ile His Asn Leu Ala His Gln Gly Val Glu Pro Ala Ser
 310 315 320 325

aca tat cct gat ctg gga ttg cct cct gaa tgg tat gga gct tta gaa 1302
 Thr Tyr Pro Asp Leu Gly Leu Pro Pro Glu Trp Tyr Gly Ala Leu Glu

Sequence Listing

330 335 340

tgg gta ttt cca gaa tgg gca agg agg cat gcc ctt gac aag ggt gag 1350
 Trp Val Phe Pro Glu Trp Ala Arg Arg His Ala Leu Asp Lys Gly Glu
 345 350 355

gca gtt aac ttt ttg aaa gga gca gtt gtg aca gca gat cgg att gtg 1398
 Ala Val Asn Phe Leu Lys Gly Ala Val Val Thr Ala Asp Arg Ile Val
 360 365 370

acc gtc agt cag ggt tat tca tgg gag gtc aca act gct gaa ggt gga 1446
 Thr Val Ser Gln Gly Tyr Ser Trp Glu Val Thr Thr Ala Glu Gly Gly
 375 380 385

cag ggc ctc aat gag ctc tta agc tcc cga aaa agt gta ttg aat gga 1494
 Gln Gly Leu Asn Glu Leu Ser Ser Arg Lys Ser Val Leu Asn Gly
 390 395 400 405

att gta aat gga att gac att aat gat tgg aac ccc acc aca gac aag 1542
 Ile Val Asn Gly Ile Asp Ile Asn Asp Trp Asn Pro Thr Thr Asp Lys
 410 415 420

tgt ctc cct cat cat tat tct gtc gat gac ctc tct gga aag gcc aaa 1590
 Cys Leu Pro His His Tyr Ser Val Asp Asp Leu Ser Gly Lys Ala Lys
 425 430 435

tgt aaa gct gaa ttg cag aag gag ttg ggt tta cct gta agg gag gat 1638
 Cys Lys Ala Glu Leu Gln Lys Glu Leu Gly Leu Pro Val Arg Glu Asp
 440 445 450

gtt cct ctg att ggc ttt att gga aga ctg gat tac cag aaa ggc att 1686
 Val Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp Tyr Gln Lys Gly Ile
 455 460 465

gat ctc att aaa atg gcc att cca gag ctc atg agg gag gac gtg caa 1734
 Asp Leu Ile Lys Met Ala Ile Pro Glu Leu Met Arg Glu Asp Val Gln
 470 475 480 485

ttt gtc atg ctt gga tct ggg gat cca att ttt gaa ggc tgg atg aga 1782
 Phe Val Met Leu Gly Ser Gly Asp Pro Ile Phe Glu Gly Trp Met Arg
 490 495 500

tct acc gag tcg agt tac aag gat aaa ttc cgt gga tgg gtt gga ttt 1830
 Ser Thr Glu Ser Ser Tyr Lys Asp Lys Phe Arg Gly Trp Val Gly Phe
 505 510 515

agt gtt cca gtt tcc cac aga ata act gca ggt tgc gat ata ttg tta 1878
 Ser Val Pro Val Ser His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu
 520 525 530

atg cca tcg aga ttt gaa cct tgc ggt ctt aat cag cta tat gct atg 1926
 Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met
 535 540 545

caa tat ggt aca gtt cct gta gtt cat gga act ggg ggc ctc cga gac 1974
 Gln Tyr Gly Thr Val Pro Val Val His Gly Thr Gly Gly Leu Arg Asp
 550 555 560 565

aca gtc gag acc ttc aac cct ttt ggt gca aaa gga gag gag ggt aca 2022
 Thr Val Glu Thr Phe Asn Pro Phe Gly Ala Lys Gly Glu Glu Gly Thr
 570 575 580

ggg tgg gcg ttc tca ccg cta acc gtg gac aag atg ttg tgg gca ttg 2070

05674824-110500

Sequence Listing

```

Gly Trp Ala Phe Ser Pro Leu Thr Val Asp Lys Met Leu Trp Ala Leu
585                                     590                                     595

cga acc gcg atg tcg aca ttc agg gag cac aag ccg tcc tgg gag ggg      2118
Arg Thr Ala Met Ser Thr Phe Arg Glu His Lys Pro Ser Trp Glu Gly
600                                     605                                     610

ctc atg aag cga ggc atg acg aaa gac cat acg tgg gac cat gcc ccg      2166
Leu Met Lys Arg Gly Met Thr Lys Asp His Thr Trp Asp His Ala Pro
615                                     620                                     625

agc agt acg agc aga tct tcg agt ggg cct tcg tgg acc aac cct acg      2214
Ser Ser Thr Ser Arg Ser Ser Ser Gly Pro Ser Trp Thr Asn Pro Thr
630                                     635                                     640                                     645

tca tgt aga cgg gga ctg ggg agg tcc aag tgc gag tct cct tca gct      2262
Ser Cys Arg Arg Gly Leu Gly Arg Ser Lys Cys Glu Ser Pro Ser Ala
650                                     655                                     660

ctg aag aca tcc tct tca tcc ttc cgc ggc ccg gaa gga tac ccc tgt      2310
Leu Lys Thr Ser Ser Ser Ser Phe Arg Gly Pro Glu Gly Tyr Pro Cys
665                                     670                                     675

aca ttg cgt tgt cct gct aca gta gag tcg caa tgc gcc tgc ttg ctt      2358
Thr Leu Arg Cys Pro Ala Thr Val Glu Ser Gln Cys Ala Cys Leu Leu
680                                     685                                     690

tgg ttc gcc ggt tcg aga aca tat gac ggc tgt gct gct gcg gcg gtg      2406
Trp Phe Ala Gly Ser Arg Thr Tyr Asp Gly Cys Ala Ala Ala Ala Val
695                                     700                                     705

aca gct tcg ggt gga cga cag tta cag ttt tgg gga ata agg aag gga      2454
Thr Ala Ser Gly Gly Arg Gln Leu Gln Phe Trp Gly Ile Arg Lys Gly
710                                     715                                     720                                     725

tgt gct gca gga tgg tta aca gca aag cac cac tca gat ggc agc ctc      2502
Cys Ala Ala Gly Trp Leu Thr Ala Lys His His Ser Asp Gly Ser Leu
730                                     735                                     740

tct gtc cgt gtt aca gct gaa atc aga aac caa ctg gtg act ctt      2547
Ser Val Arg Val Thr Ala Glu Ile Arg Asn Gln Leu Val Thr Leu
745                                     750                                     755

tagccttagt gattgtgaag tttgttgctt tctgtgtatg ttgtcttgct cttagctgac      2607

aaatatattga cctgttgagg aattttatct ttgctgctgt ttttttttaa tcaaaagagg      2667

gggtttcctc cgatttcatt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      2727

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa      2771

<210> 2
<211> 756
<212> PRT
<213> Triticum aestivum

<400> 2

Met Ala Ala Thr Gly Val Gly Ala Gly Cys Leu Ala Pro Ser Val Arg
1 5 10 15

```

0364-4069-110600

Page 5

Sequence Listing

Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His Ala Ser
 275 280 285
 Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly Val Tyr
 290 295 300
 Arg Asp Ser Arg Ser Thr Leu Val Ile His Asn Leu Ala His Gln Gly
 305 310 315 320
 Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro Glu Trp
 325 330 335
 Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg His Ala
 340 345 350
 Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val Val Thr
 355 360 365
 Ala Asp Arg Ile Val Thr Val Ser Gln Gly Tyr Ser Trp Glu Val Thr
 370 375 380
 Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser Arg Lys
 385 390 395 400
 Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp Trp Asn
 405 410 415
 Pro Thr Thr Asp Lys Cys Leu Pro His His Tyr Ser Val Asp Asp Leu
 420 425 430
 Ser Gly Lys Ala Lys Cys Lys Ala Glu Leu Gln Lys Glu Leu Gly Leu
 435 440 445
 Pro Val Arg Glu Asp Val Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp
 450 455 460
 Tyr Gln Lys Gly Ile Asp Leu Ile Lys Met Ala Ile Pro Glu Leu Met
 465 470 475 480
 Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro Ile Phe
 485 490 495
 Glu Gly Trp Met Arg Ser Thr Glu Ser Ser Tyr Lys Asp Lys Phe Arg
 500 505 510
 Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr Ala Gly
 515 520 525

00674624-110600

Sequence Listing

Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn
 530 535 540
 Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His Gly Thr
 545 550 555 560
 Gly Gly Leu Arg Asp Thr Val Glu Thr Phe Asn Pro Phe Gly Ala Lys
 565 570 575
 Gly Glu Glu Gly Thr Gly Trp Ala Phe Ser Pro Leu Thr Val Asp Lys
 580 585 590
 Met Leu Trp Ala Leu Arg Thr Ala Met Ser Thr Phe Arg Glu His Lys
 595 600 605
 Pro Ser Trp Glu Gly Leu Met Lys Arg Gly Met Thr Lys Asp His Thr
 610 615 620
 Trp Asp His Ala Pro Ser Ser Thr Ser Arg Ser Ser Ser Gly Pro Ser
 625 630 635 640
 Trp Thr Asn Pro Thr Ser Cys Arg Arg Gly Leu Gly Arg Ser Lys Cys
 645 650 655
 Glu Ser Pro Ser Ala Leu Lys Thr Ser Ser Ser Ser Phe Arg Gly Pro
 660 665 670
 Glu Gly Tyr Pro Cys Thr Leu Arg Cys Pro Ala Thr Val Glu Ser Gln
 675 680 685
 Cys Ala Cys Leu Leu Trp Phe Ala Gly Ser Arg Thr Tyr Asp Gly Cys
 690 695 700
 Ala Ala Ala Ala Val Thr Ala Ser Gly Gly Arg Gln Leu Gln Phe Trp
 705 710 715 720
 Gly Ile Arg Lys Gly Cys Ala Ala Gly Trp Leu Thr Ala Lys His His
 725 730 735
 Ser Asp Gly Ser Leu Ser Val Arg Val Thr Ala Glu Ile Arg Asn Gln
 740 745 750
 Leu Val Thr Leu
 755

<210> 3

<211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(22)
 <223> primer

<400> 3
 cctcccaatt caaggattag tg

22

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial Sequence, Primer

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> primer

<400> 4
 cctcgcatgc agcatagcaa

20

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial Sequence, primer

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> primer

<400> 5
 tgtggctgca agtgaggagg

20

<210> 6
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)..(23)
 <223> primer

<400> 6
 ccagtcacaa acacgtagct acg

23

00907F" 42342960